11:10:45:23 2004

us-09-901-910-2.rapb

Page 1

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

August 31, 2004, 18:25:19 ; Search time 127 Seconds
(without alignments)
943.839 Million cell updates/sec

protein search, using sw model

US-09-901-910-2

1 MSSRIARALALVVTLLHLTR.........ANEAAPFYFRLFNDIHKFRD 381

score: 2115

table: BIOSUM62
Gapop 10.0 , Gapext 0.5

called: 1297172 seqs, 314612898 residues

Minimum number of hits satisfying chosen parameters: 1297172

minimum db seq length: 0
maximum db seq length: 200000000

processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US05_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

SUMMARIES

% Query	Match	Length	DB	ID	Description
100.0	381	10	US-09-901-910-2	Sequence 2, Appli
100.0	381	14	US-10-294-796-2	Sequence 2, Appli
100.0	381	14	US-10-044-564-41	Sequence 2, Appli
100.0	381	15	US-10-394-015-5	Sequence 5, Appli
100.0	381	15	US-10-099-322-42	Sequence 42, Appl
100.0	381	15	US-10-044-564-42	Sequence 42, Appl
100.0	381	16	US-10-381-644-2	Sequence 2, Appl
100.0	381	16	US-10-464-368-61	Sequence 61, Appl
100.0	455	16	US-10-312-459-2	Sequence 2, Appli
99.9	381	9	US-09-925-301-1432	Sequence 1432, Ap
99.9	381	15	US-10-099-322-43	Sequence 43, Appl
99.7	381	15	US-10-044-564-43	Sequence 43, Appl
99.7	381	15	US-10-099-322-45	Sequence 45, Appl
99.7	381	15	US-10-044-564-44	Sequence 44, Appl
99.6	381	14	US-10-205-023-84	Sequence 84, Appl
99.6	381	15	US-10-099-322-2	Sequence 2, Appli

Red No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

RESULT 1
US-09-901-910-2

Sequence 2, Application US/09901910
Publication No. US20030012768A1
GENERAL INFORMATION:
APPLICANT: Li, Haodong
APPLICANT: Adams, Mark
APPLICANT: Calenda Valerie
TITLE OF INVENTION: Connective Tissue Growth Factor-2
FILE REFERENCE: PF12FP2
CURRENT APPLICATION NUMBER: US/09/901,910
CURRENT FILING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: 09/348,815
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: 08/459,101
PRIOR FILING DATE: 1995-06-02
PRIOR APPLICATION NUMBER: PCT/US94/07736
PRIOR FILING DATE: 1994-07-12
PRIOR APPLICATION NUMBER: 60/217,402
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 60/291,642
PRIOR FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.0

SEQ ID NO 2
LENGTH: 381
TYPE: PRT
ORGANISM: homo sapiens
US-09-901-910-2

Query Match 100.0%; Score 2115; DB 10; Length 381;
Best Local Similarity 100.0%;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ALIGNMENTS

Qy 1 MSSRIARALALVVTLLHLTRIALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL 60
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 MSSRIARALALVVTLLHLTRIALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL 60

16	2107	99.6	381	15	US-10-099-322-41	Sequence 41, Appl
17	2107	99.6	381	15	US-10-044-564-2	Sequence 2, Appli
18	2107	99.6	381	15	US-10-044-564-41	Sequence 41, Appli
19	2106	99.6	381	13	US-10-053-753-4	Sequence 4, Appli
20	2106	99.6	381	15	US-10-182-432-4	Sequence 4, Appli
21	2106	99.6	381	15	US-10-312-459-6	Sequence 6, Appli
22	1980.5	93.6	374	9	US-09-853-625B-12	Sequence 12, Appli
23	1980.5	93.6	375	10	US-09-901-910-7	Sequence 7, Appli
24	1938	91.6	379	9	US-09-853-625B-11	Sequence 11, Appli
25	1938	91.6	379	13	US-10-053-753-2	Sequence 2, Appli
26	1938	91.6	379	15	US-10-099-322-45	Sequence 45, Appli
27	1938	91.6	379	15	US-10-182-432-2	Sequence 2, Appli
28	1938	91.6	379	15	US-10-044-564-45	Sequence 45, Appli
29	1938	91.6	379	16	US-10-464-368-60	Sequence 60, Appli
30	1938	91.6	379	16	US-10-627-604-11	Sequence 11, Appli
31	1937	91.6	379	16	US-10-464-368-62	Sequence 62, Appli
32	1699	80.3	375	9	US-09-853-625B-13	Sequence 13, Appli
33	1699	80.3	375	16	US-10-627-604-13	Sequence 13, Appli
34	1667.5	78.8	375	16	US-10-464-368-63	Sequence 63, Appli
35	1348	63.7	375	16	US-10-627-604-12	Sequence 12, Appli
36	959	45.3	347	14	US-10-245-977-7	Sequence 7, Appli
37	959	45.3	347	16	US-10-464-368-56	Sequence 56, Appli
38	957	45.2	348	14	US-10-390-986-2	Sequence 2, Appli
39	957	45.2	348	13	US-10-101-040-3	Sequence 3, Appli
40	956.5	45.2	348	16	US-10-627-604-15	Sequence 15, Appli
41	952.5	45.0	348	9	US-09-853-625B-15	Sequence 15, Appli
42	952.5	45.0	348	13	US-10-053-753-6	Sequence 6, Appli
43	952.5	45.0	348	14	US-10-245-977-8	Sequence 8, Appli
44	952.5	45.0	348	15	US-10-182-432-6	Sequence 6, Appli
45	952.5	45.0	348	16	US-10-464-368-54	Sequence 54, Appli

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

protein - protein search, using sw model

h on: August 31, 2004, 18:20:27 ; Search time 57 Seconds
                                           (without alignments)
                                           1888.607 Million cell updates/sec

ple: US-09-901-910-2
fect score: 2115
uence: 1 MSSRIARALALVVTLLHLTR.........ANEAAFPYRLFNDIHKFRD 381

ring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5
rched: 1586107 seqs, 282547505 residues

al number of hits satisfying chosen parameters: 1586107

imum DB seq length: 0
imum DB seq length: 200000000

t-processing: Minimum Match 0%
               Maximum Match 100%
               Listing first 45 summaries

base :   A_Geneseq_29Jan04:*
               1: geneseqp1980s:*
               2: geneseqp1990s:*
               3: geneseqp2000s:*
               4: geneseqp2001s:*
               5: geneseqp2002s:*
               6: geneseqp2003as:*
               7: geneseqp2003bs:*
               8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
1	2115	100.0	381	2	AAW35957	Aaw35957 Human mon
2	2115	100.0	381	4	AAB90773	Aab90773 Human she
3	2115	100.0	381	5	AAU79761	Aau79761 Human Cyr
4	2115	100.0	381	5	ABB05438	Abb05438 Human Cyr
5	2115	100.0	381	6	AAE18107	Aae18107 Human con
6	2115	100.0	381	6	ABU63222	Abu63222 Human con
7	2115	100.0	455	3	AAB43987	Aab43987 Human can
8	2107	99.6	381	3	ABG76937	Abg76937 Human pro
9	2107	99.6	381	7	ADB75260	Adb75260 Prostate
10	2106	99.6	381	2	AAW35730	Aaw35730 Human cys
11	2106	99.6	381	4	AAE05921	Aae05921 Human cys
12	1980.5	93.6	374	4	ABB09202	Abb09202 HCGF CNN
13	1980.5	93.6	375	2	AAR90919	Aar90919 Connectiv
14	1980.5	93.6	375	5	AAY31620	Aay31620 Human CTG
15	1980.5	93.6	375	6	AAE18108	Aae18108 Human alt
16	1980.5	93.6	375	6	ABU63223	Abu63223 Human con
17	1938	91.6	375	2	AAR25565	Aar25565 Beta-IG-M
18	1938	91.6	379	4	AAE05920	Aae05920 Mouse cys
19	1938	91.6	379	5	ABB09201	Abb09201 Mouse cyr
20	1699	80.3	375	4	AAE05939	Aae05939 Chicken C
21	1699	80.3	375	5	ABB09203	Abb09203 Chicken c
22	959	45.3	347	6	ABR43138	Abr43138 Rat conne
23	957	45.2	347	6	AAY24379	Aay24379 Rat conne
24	956.5	45.2	348	2	AAR25566	Aar25566 Beta-IG-M
25	956.5	45.2	348	6	ADB25766	Adb25766 Mouse con
26	956.5	45.2	348	6	ADB25762	Adb25762 Mouse con
27	952.5	45.0	348	2	AAW35731	Aaw35731 Murine Fi
28	952.5	45.0	348	4	AAY44756	Aay44756 Mouse con
29	952.5	45.0	348	5	AAE05922	Aae05922 Mouse fib
30	952.5	45.0	348	5	ABB09205	Abb09205 Fisp-12 C
31	952.5	45.0	348	6	ABR43139	Abr43139 Mouse con
32	952	45.0	347	2	AAW12694	Aaw12694 Connectiv
33	952	45.0	347	3	AAY93340	Aay93340 Amino aci
34	951	45.0	349	2	AAR79964	Aar79964 Connectiv
35	951	45.0	349	2	AAW11302	Aaw11302 Connectiv
36	951	45.0	349	2	AAW09089	Aaw09089 Human con
37	951	45.0	349	2	AAW62084	Aaw62084 Human con
38	951	45.0	349	2	AAW81425	Aaw81425 Connectiv
39	951	45.0	349	3	AAY18361	Aay18361 Human con
40	951	45.0	349	3	AAY92939	Aay92939 Human con
41	951	45.0	349	3	AAY92940	Aay92940 Human con
42	951	45.0	349	3	AAY44755	Aay44755 Human con
43	951	45.0	349	4	AAB84598	Aab84598 Human aci
44	951	45.0	349	4	AAB90791	Aab90791 Human she
45	951	45.0	349	4	AAB60664	Aab60664 Human con

ALIGNMENTS

RESULT 1
AAW35957

```
ID   AAW35957 standard; protein; 381 AA.
XX
AC   AAW35957;
XX
DT   05-MAR-1998  (first entry)
XX
DE   Human monocyte mature differentiation factor.
XX
KW   Human; monocyte; mature; differentiation factor; MMDF; macrophage;
KW   cancer; immune activator; tissue culture; infectious disease.
XX
OS   Homo sapiens.
XX
XX
PN   JP09234079-A.
XX
PD   09-SEP-1997.
XX
PF   04-MAR-1996;   96JP-00075236.
XX
PR   04-MAR-1996;   96JP-00075236.
XX
PA   (TOYM ) TOYOBO KK.
XX
DR   WPI; 1997-497320/46.
DR   N-PSDB; AAT97142.
XX
PT   A monocyte mature differentiation factor - useful for the long term
PT   tissue culture of macrophage(s).
PS   Claim 9; Page 12-13; 22pp; Japanese.
XX
CC   The present sequence represents a monocyte mature differentiation factor
CC   (MMDF) which maintains the life of macrophages for long periods in liquid
CC   culture. MMDF can be used as an anti-cancer agent, an immune activator
CC   and to treat infectious diseases
XX
SQ   Sequence 381 AA;

Query Match              100.0%;  Score 2115;  DB 2;  Length 381;
Best Local Similarity    100.0%;
Matches    381;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy      1 MSSRIARALALVVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MSSRIARALALVVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGCGCCKVCAKQL 60
```